

Molecular Biology

THE SEARCH FOR GENES INVOLVED IN BACTERIAL LEAD RESISTANCE

Laura Kulhanek, Beth Gummersheimer and Tara Giblin*

Department of Natural Sciences, Stephens College, Columbia, MO 65215

tgiblin@stephens.edu

Lead contamination is a problem in eastern Missouri, an area often termed the “lead belt”. Lead may accumulate in soil, posing a hazard for children in contact with the soil. Ingestion of bioavailable lead causes lead poisoning, which leads to impairment of mental function. Lead is classified as a persistent contaminant, since it binds tightly with the soil. Land that is left untreated will continue to be hazardous for many years. Current methods of cleanup can be costly and ineffective for long term treatment. One possible method of cleanup is the use of lead altering bacteria.

Bacteria tolerate heavy metals in their environment through several mechanisms, including sequestration or efflux of the metal or through chemical modification to create a less toxic metal form. Presently, the genetic factors involved in bacterial lead resistance are largely unknown. While genes for other metal resistances have been discovered, only one gene involved in lead resistance has been cloned. Finding the genes involved in bacterial detoxification of lead is important in pinpointing a bacterial strain that may diminish the toxicity of lead.

Two bacterial strains were isolated from lead contaminated soil obtained near a lead smelter. They belong to the genera *Corynebacterium* and *Pseudomonas*, and are resistant to 2 millimolar (mM) lead as well as other metals. A DNA library has been created from the gram positive, *Corynebacterial* strain to look for possible lead resistance genes. Recombinant clones were screened for the ability to confer bacterial resistance to cadmium, cobalt, zinc, copper, lead or mercury. DNA inserts were isolated from clones that showed high levels of resistance to cadmium, lead and mercury. The inserts range in size from 2 to 4 kilobases. Future plans include sequencing the DNA inserts to determine whether they encode for known proteins.